

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

## **REPLACEMENT SHEET**

1/27



448 KD G1 i-antigen : protein and nucleic acid sequences

+1321 TEATRIGRATTA

Fig. 1

REPLACEMENT SHEET

2/27

G5 Wild-type	
SEQ ID NO: 44	10 ATGAAAAATA ATTATTTGAT AATATTGATT ATTCAATTAT TTATCAATAA 50 AATTTAAATT CCTTAATTGTT CCTTAATTGTC 60 CTTTGAAAC TGAACATAC 70 ACAGGGAT AAGTTGATGA 80 TCTAGGAACT
	130 140 150 160 170 180 190 200 210 220 230 240
	CCTGCAAATT GTGTAAATTG TTAGAAAAC TTATTTATA ATAATGCTGC TGCTTCTTT CCTGGTCTA GAACTGTAC 300 ACCTTGTCGA TAAACCAAT
	250 260 270 280 290 300 310 320 330 340 350 360
	CCACCTCTTA CTGCTTAATT AGTCACATTA TTTAAACCTTA AATGCCCTTC TGTTTACCGCA ATTGCAAGTG GAGCAACAGA TTATCCAGCA ATAACTACAG AAATTTAAAG ATGCTGGTGC TTAAACCAAT
	370 380 390 400 410 420 430 440 450 460 470 480
	AATTUTTATA ATGAAATTC TCCAAATTTC TTCAAAATTTC AATGCAAGTG CTAGTACATG CACAGCTGT CGGGTAACAA GAGTTGGGG TGCTATTGACT GCTGTAAATG CGGTAACTAT AGTCGATATAA
	490 500 510 520 530 540 550 560 570 580 590 600
	TGTTAACCTG CATSTCCTAC TGGTACTGGC CTTGATGATG GAGTAACTAC TGTTATGTT AGATCATTC CAGAATCTGT TAATTTGTA CTTAACTTT ACTATATGG TAATATGG TAATATGG
	610 620 630 640 650 660 670 680 690 700 710 720
	AATATCTCTT TCAATCCGG TAAATGTTA TCCACCCCTT GTCCGGCAT TAACCTCTT AATGTTGCTT AGCTTACTTT AGCTTAACTT GCTACATTA CGCTACATTA CGCTACATTA CGCTACATTA
	730 740 750 760 770 780 790 800 810 820 830 840
	TGCCCTGATG GTACTATAG TGCTCTGCA GTAAATTAATG GGTAGGCA AAACACTGA TGTTACTATT GTGCTCTAA CTTTACAT AATATGCTC CTTATTCAA TCCAGGTTAT
	850 860 870 880 890 900 910 920 930 940 950 960
	ATGACTGCC TACCTGCC AGCAAAATAA GATTATGGTG CTGAAGGCCAC TGCGGGTGT GCGCGTACTT TAGCCAAATA ATCTTATTT GCATGCCCTG ATGGTACTGC AATTGGCTGT
	970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
	GGAGGACTA ATTATGAAAT ATTATAAACA GAATGCTAA ATGTTGTCG TAACCTTTAT TTGATGGTA ATTATCTCA GGCGGGAGT AGTATGCGA AAGCATGTCG AGCAATTA
	1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
	CTTTAAGGGC CTGAGAAC TCCAGGTCTT ACTGCTACTT TAATTTGATA ATGCTGCTT GAATCCCTG CTGGTACTGT ACTCAGCGAT GGAACAACT CTACTATATA ATTAGGAGCA
	1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
	TGTTAATGIG TAAATGIG TGCCAACTTT TATACTACAA AATTAACGTA TTGGTACCA GGTATTGATA CTGGTACTAG TTGTTATAAA AATTTAACTT CTGGCCCTGA AGCTTAATTA
	1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
	CCTGAACTCG CTAAAGAAA TATATAATG GATTGGCTA ATTTTTATC AATTTCCCTA TTATGTTT CTTATGTTT ATTATGTT ATTATGTA .....

Coding region: nucleotides 1-1404

Fig: 2a

REPLACEMENT SHEET

3/27



G5 SYNTHETIC

SEQ ID NO: 102	10	20	30	40	50	60	70	80	90	100	110	120
ATGAAAGAAC	ATCATCTCTGT	GATCCTGTC	ATCTCTCTGT	TCATCAACCA	GATCAAGCTT	GCTAACTTC	CTCTGGAAAC	CGAGACCAAC	ACCGTGGAC	AGGTGACGA	CTCTGGAAAC	
130	140	150	160	170	180	190	200	210	220	230	240	
CCTGCTTA	CTGTGAACTG	TGAGAAGAAC	TCTACTACCA	ACACCCCTGC	TGCTTTCGTC	CCCTGGACCTT	CTAACCTGAC	CCCTTGTCT	CAGAAGAAG	ACGGCTGAGC	TGACCTAAC	
250	260	270	280	290	300	310	320	330	340	350	360	
CTCTCTGCTA	CCCTCAACTT	GGTACCCCG	TGTAAGCTG	AGTGTCTGC	TGGAACCGT	ATCGTGGG	GGCTTGGGA	CTAGCTGCT	ATCATCACCG	AGTGTTGAA	CTCTGGATC	
370	380	390	400	410	420	430	440	450	460	470	480	
AACTCTTACA	ACCGAGACG	TCCTAACCTC	AACCGTGGAG	CTTCTACTCT	TACCGCTTCT	CCCTGAAACC	GGGTGGAGG	AGCTCTGAC	GCTGGAAAAG	CTGGTACCAT	CGTGGCTAG	
490	500	510	520	530	540	550	560	570	580	590	600	
TGTAAGCTG	CTGTCCTAC	CGGAACTCT	CTGGAGAGC	GTGTAACAC	CGGCTAATG	CGCTTCTTCA	CGGAGTGTGT	GTGAGTGTG	CTGAACTTCT	ACTACACGG	AAACAAACGA	
610	620	630	640	650	660	670	680	690	700	710	720	
AAACCCCTT	TCAACCCCTG	AAAGCTCTAG	TGTAACCTCT	GTGCTCTAT	CAAGCTCTCT	AACTGGCTC	AGCTGCTGCT	GGAAACCCCT	GCTACATCA	CGCTCTAGTG	TAACGTCCT	
730	740	750	760	770	780	790	800	810	820	830	840	
TGTCCTGAG	GAACCTTC	TGCTCTCTGA	GTGAACTCT	GGTGGCTCA	GAACACCGAG	TGTAACAACT	GTGCTCTTAA	CTTCTACAC	AACAGCTTC	CTAACCTTCA	CCCTGGAAAC	
850	860	870	880	890	900	910	920	930	940	950	960	
TCTAACCTGTC	TCCCTCTCC	TGCTTAACAG	GAATCTGAG	CTGAGCTTAC	CGCTGGAGA	GCTCTAACCC	TGCTTAAGCA	GCTAACTAC	GCTGTCTG	ACGGAAACCG	TATGGCTCT	
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	
GGAGCTTACCA	ACTACGTTAT	CCTCAGAACCC	GAGTGTCTGA	ACTGTCTGC	TAATCTTAC	TTGGAGGAA	ACAACTTCA	GGCTGGATCT	TCTCTGTA	AGGCTTGTC	TGCTAACAG	
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	
GTCAGGGAG	CTCTGGCTAC	CGCTGGAGA	ACCCCTAACCC	TGATGCTCA	GTGCTCTG	GTGCTGCTG	CTGGAACCT	GTGCTGCT	CTAACCTAC	CGAGCTGCT		
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	
TCTCTGCTG	TGAGTGTGC	TGCTTAACCTC	TACACCACCA	AGCAGACCA	CTGGCTGCT	GGATGCTCA	CCTGTTACCTC	TGTTAAAG	AAAGTGAACCT	CTGGGCTGTA	GGCTAACCTG	
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	
CCTGAGTC	CTAAGAGAA	CATCAGCTG	GAATCTGCTA	ACTCTCTTC	TATCTCTG	CTGCTGCT	CTTACTACCT	CTCTGTTATA	.....	.....	.....	

Coding region: nucleotides 1-1404

Fig. 2b



Title: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF ICHTHYOPHTHIRIUS  
Applicant(s): CLARK et al.  
Serial No.: 09/497,967

Filed: February 4, 2000

Docket: 235.0017 0101

Sheet 5 of 27

**REPLACEMENT SHEET**

5/27



*Fig. 3b<sub>1</sub>*

*Fig. 3b<sub>2</sub>*

*Fig. 3b*

REPLACEMENT SHEET

6/27

Fig. 3b<sub>1</sub>

Sequence Alignment of 48 kD G1 i-antigen  
and 55 kD G5 i-antigen nucleotide sequences

G1 SEQ ID NO: 1 ATGAAATATAATTTTATTAAATTAAATTATTCTTTATTATTAAATGAATTAAGAGCT  
G5 SEQ ID NO: 3 ATGAAAAATAATATTTAGTAATATTGATTATTCAATTAAATTAAATCT

G1	G5	GTTCCATGCTCTGATGGTACTTAGACTCA---AGCTGGAT---TGACTGATGTAGGTGC
		GCTAATGCTCTGGAACTGAAACTAACACAGCCGGATAAGTTGA-TGATCTAGGAAC
G1	G5	TGCTGATCTGGTACTTGTGTTAATTGC-AGACCTAATTTTACTATAATGGTGGTGCCTG
		TCCT-----GCAAATTGTGTTAATTGTTAGAAA-AACTTTATTATAATGCTGCTG
G1	G5	CTTAAGGAGAAGCTAATGGTAATTAAACCTTCGCAGCAAATAATGCTGCTAGAGGTATAT
		CTT-----TCGTTCC-----TGGTGCTAG---TACGT
G1	G5	GTGTACCATG-CCA-AATAAACAGA-GTAGGCTCTGTTACCAA-TGCAGGTG--ACTTAG
		GTACACCTTGTCCATAAAAAAAAGATGCTGGTGC-TAACCAAATCCACCTGCTACT--G
G1	G5	CTACTTTAGCCACATAATGCAGTACTTAATGTCCTACTGGCACTGCACTTGATGATGGAG
		CTAATTTAGTCACATAATGTAACGTAAATGCCCTGCTGGTACCGCAATTGCAAGGTGAG
G1	G5	TGACAGATGTTTTG--ATAGATCAGCCGCATAATGTTAAATGCAAACCTAACCTTA
		CAACAGATATTGCAAGAATA-ATCA---CAGAATGTTAATTGTTAGAATTAAATTGTTA
G1	G5	CTATAATGGTGGTCTCCTTAAGGTGAAGCTCCCTGGCTTTAAGTTTTGCTGCTGGTGC
		--TAATGA-----AA---ATGCTCC-----AAATTTAA-----
G1	G5	TGCCGCTGCAGGTGTTGCTGCCGTTACTAGTTAATGTTACCTTGCCAACTAAACAAAA
		-----TGCAGGTG-----CTAGTACATGCACAGCTTGTCCGGTAAACAGAGT
G1	G5	CGATTCTCTGCCACTGCAGGT---GCCTAAGCTAATTAGCCACATAATGTTAGCAATT
		TGGTGGTGCATTGACTGCTGGTAATGCC---GCTACCATAGTCGCATAATGTAACGTCGC

REPLACEMENT SHEET

7/27



G1	ATGTCCTACTGGCACTGTACTTGATGATGGAGTGACACTTGT	TTTAATACATCAGCCAC
G5	ATGTCCTACTGGTACTGCACTTGATGATGGAGTAAC	ACTACTGATTATGTTAGATCATT
G1	ATTATGTGTTAAATGCAGACCTA	CTCCTTA
G5	TTTACTATAATGGT-----GGTT	AGAATGTGTTAAATGTAGACTTA
G1	-----AGGTGAA-----	GCTCCTGGCGTTA
G5	CAATCCAGGTAAGTTAATGCACACCTTGTCCGGCAATTAAAC	CTGCTAATGTTGCTTA
G1	AG-----TTT-----	TTGC-----TGCTGG
G5	AGCTACTTTAGGTAATGATGCTACAATAACCGATA	ATGTAACGTTGCATGCCCTGATGG
G1	TGCT-----GCCGCTGCAG-----	GTGTTGC-----
G5	TACTATAAGTGCCTGCTGGAGTAATAATTGGGTAGC	ACAAAACACTGAATGTAATTG
G1	-----TGCCGTTACTAGTTAATGTGT-----	TGCTCCTAACTTTACAATAATAATGCTCCTAATTCAATCCAGGTAATAGTACATGCC
G5	TGCTCCTAACTTTACAATAATAATGCTCCTAATTCAATCCAGGTAATAGTACATGCC	-----
G1	ACCTTGCCAAATAAACAAAACGATTCTCCTG-----	CCACTGCAGGTGCTAAAGCTAATT
G5	ACCTTGCCCAAGCAAATAAAGATTATGGTGC	TAAGCCACTGCAGGTGGTGGCTACTTT
G1	AGCCACATAATGCAGTACTTTAATGTC	AAAGACGGAGTGACAC
G5	CAACTGGTAAATGTAATATTGCA	TGCATGCCCTGATGGTACTGCAATTGCTAGT-GGAGCAAC-----
G1	TTGTTTTAGTAAT-TCATCCACATAATGTTCTTAAT-GCATTGCTAATTACTTTTTAA	-TAATTAT-GTAATTATAAACAGAATGT-CTAATTGCTGCTAACTTTATTGAA
G5	-TAATTAT-GTAATTATAAACAGAATGT-CTAATTGCTGCTAACTTTATTGAA	-----
G1	TGGTAAT-----TTCGAAGCAGGTAAAAGTTAATGTTAAAG-----	TGTCAGTAAGTAAAAC
G5	TGGTAATAATTCTAGGCAGGAAGTAGATGC-----	AAAGCATGTCAGCAAATAAAGTT
G1	A-----CTCCAGCACATGCTCCAGGTAAACTGCTACTTAAGCCACATAATGT-----	TT
G5	TAAGGCCTGTAGCAA-----CTGCAGGTGGTACTGCTACTTTATTGCAATGTGCC	TT
G1	GACCACATGCTCTGCTGGTACAGTACTTGATGATGGAA	CATCAACTAATTGTAGCTTC
G5	GA-----ATGCCCTGCTGGTACTGTA	ACTCACCGATGGAACACATCTACTTATAAAATAAGC
G1	CGCAACTGAATGTA	TTAAATGTCGCTGGCTTTTGCA
G5	TTAAATGTCGCTGGCTAACTTACTACAAAATAACTGATTGGGT	-----
G1	AGCAGGTACTGATA	CATGTAACCTCTGGTGGCCACAGCTAA
G5	CATGTAACCTCTGGTGGCCACAGCTAA	-----
G1	AGTATATGCTGAAGCTACTCAAAAAG-----	TATAATGCGCCTCCACTACTTCGCTAAATT
G5	TTTAC-----CTGAATCTGCTAAAAAAATATAATGTG-----	ATTTCGCTAAATT
G1	TTTATCGATTCCCTATTATTATTCTTTCTATTATTG	
G5	TTTATCAATTCCCTATTATTGATTCTTATTATTATTAA	

Fig. 3b<sub>2</sub>

**REPLACEMENT SHEET**

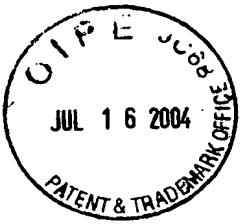
8/27



55 KD i-antigen protein

SEQ ID NO: 7 MKNNILVILI ISLFINQIKS ANC P VGTETN TAG QV DDLGT PANC VNC QKN FYY NNAA AFV  
PGAST CTPCP QKK DAGA QPN PPATANL VLTQ CNVK C PAGTA IAGGAT DYAA II TEC VNC RI  
NFYNENAPNF NAGAST C TAC PVNRVGGALT AGNAATIVAQ CNVAC P TIGTA LDDGV TTDYV  
RSFTECVKCR LNFYYNGNNG NTPFNP GKSQ CTPC PAIKPA NVAQATLGND ATITAQCNVA  
CPDGTISAAG VNNWVAQNT E CTNCA PNF YN NNAPNFNP GNG STCLPCPANK DYGA EA TAGG  
AATLAKQCNI ACPDGTAIAS GATNYVILQT ECLNCAANFY FDGNNFQAGS SRCKACPANK  
VQGAVATAGG TATLIAQCAL ECPAGTVLTD GTTSTYKQAA SECVKCAANF YTTKQTDWVA  
GIDTCTSCNK KLTSGAEANL PESAKKNIQC DFANFLSISL LLISYYLL\*\* .....  
10 20 30 40 50 60  
70 80 90 100 110 120  
130 140 150 160 170 180  
190 200 210 220 230 240  
250 260 270 280 290 300  
310 320 330 340 350 360  
370 380 390 400 410 420  
430 440 450 460 470 480

*Fig. 4*



48 KDa G1 i-antigen repeats

SEQ ID NO: 10  
8 CPPTGTAATGQVDDLGTPANCVNCQKNFYXNNAA---AFVPGASTCTCPCHQKIDAGAQOPNPPATENLVT-OCNVK  
9 CPTGTAALDDGVTPTDVSAAQCVKCKPNFYXNGGSPGEAHCVOVFNAGAAPPAAAVTSQCVPCOLAMNDSPATAGQA---NLATOCSTQ  
10 CPTGTVLDGVTPTDVSATLCKKCKPNFYXNGGSPGEAHCVOVFNAGAAPPAAAVTSQCVPCOLAMNDSPATAGQA---NLATOCSTQ  
11 CPTGTAALPGVTPTDVSATQCVPCOLAMNDSPATAGQA---NLATOCSTQ  
12 CPTGTAALPGVTPTDGSATEDKCSACFFASKTRG-FPA---NLATOCSTQ  
\* \* \*

Fig: 5a

9/27

55 kDa G5 i-antigen repeats

SEQ ID NO: 55 1  
CPVGTETNTAGQVDDLGTPANCVNCQKNFYXNNAA---AFVPGASTCTCPCHQKIDAGAQOPNPPATENLVT-OCNVK  
56 2 CPAGTAAITGG-ATPDVAATITTECVNCRINFYNNAP---NFNAGASTCTTACHVNRVGGATAGNAATIV---AQCNVA  
57 3 CPTGTAALDDGVTTDVSFTTECVCRINFYNNAP---CPNPGKRSQCTPCPAIKPANVAQATLGNDAITTAQCNVA  
58 4 CPDGTTSAAGVNNVAQN-TECTINCAPNFYNNAP---NMPGNSTCPCPANDGAEATAGGATLAK-QCNVA  
59 5 CPDGTAALISGATINVILQ-TECTINCAPNFYNNAP---NEQAGSSRQKACPANVQGAVATAGGATLII-AQCALE  
60 6 CBAGTIVLTDGMSITKQAASECVIRCAANFYTTKQ---TDWVAGIDCTSCNKKLTSGAZBANLPESAKKNI-QCDEFQ  
\* \* \*

Fig: 5b

10/27

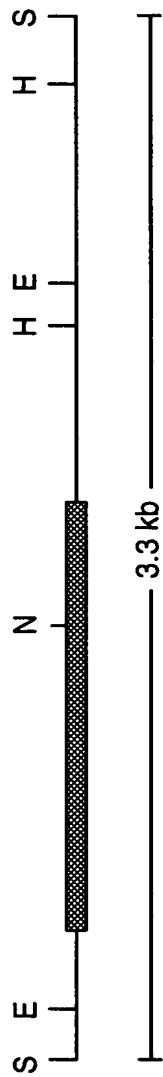


Fig. 6

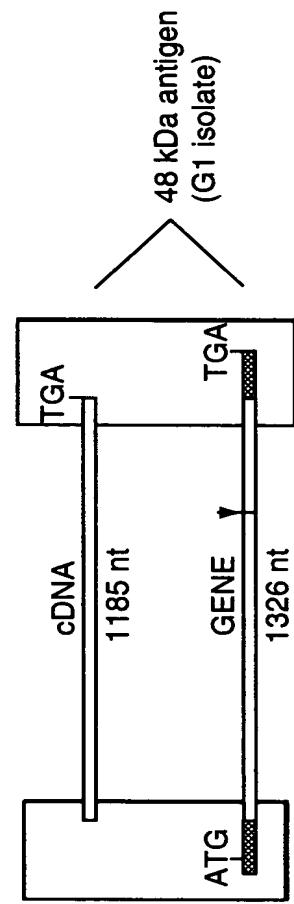


Fig. 7a



11/27

897 L CTC ... TTC F 952

1.172

CDNA GENE

1227

Fig. 7b

**REPLACEMENT SHEET**

12/27



Fig. 8

13/27

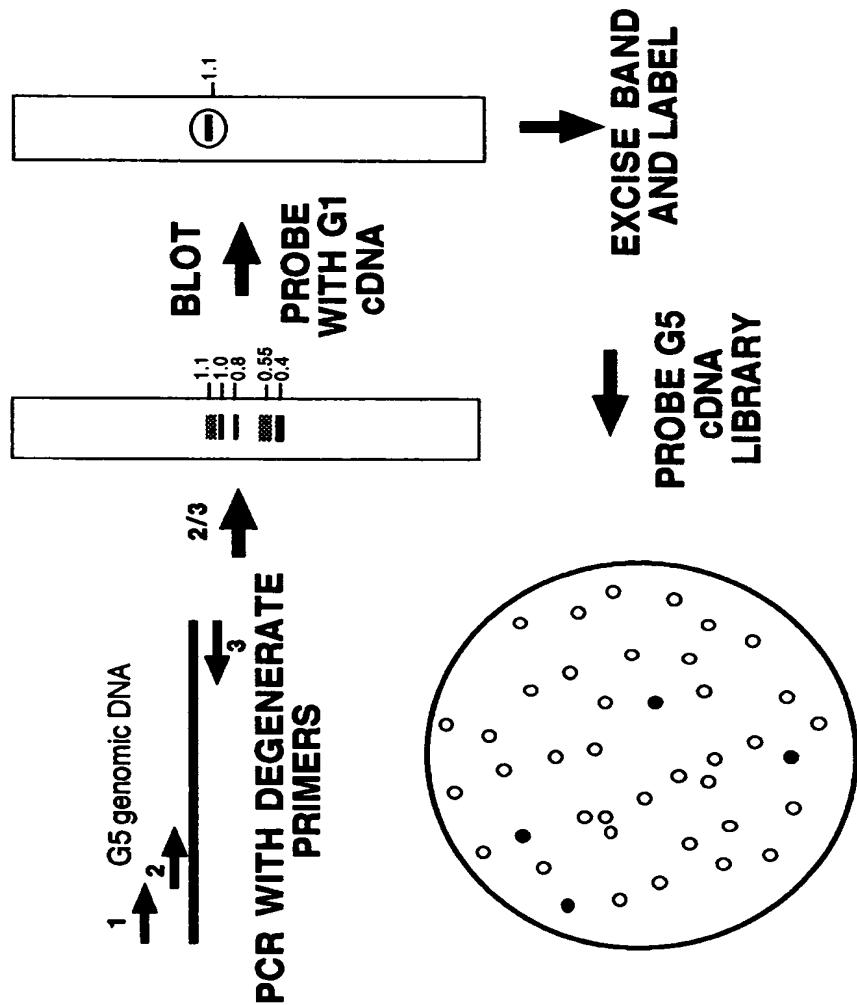
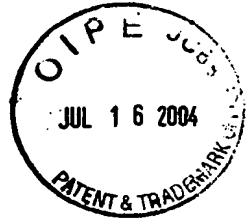


Fig. 9



14/27

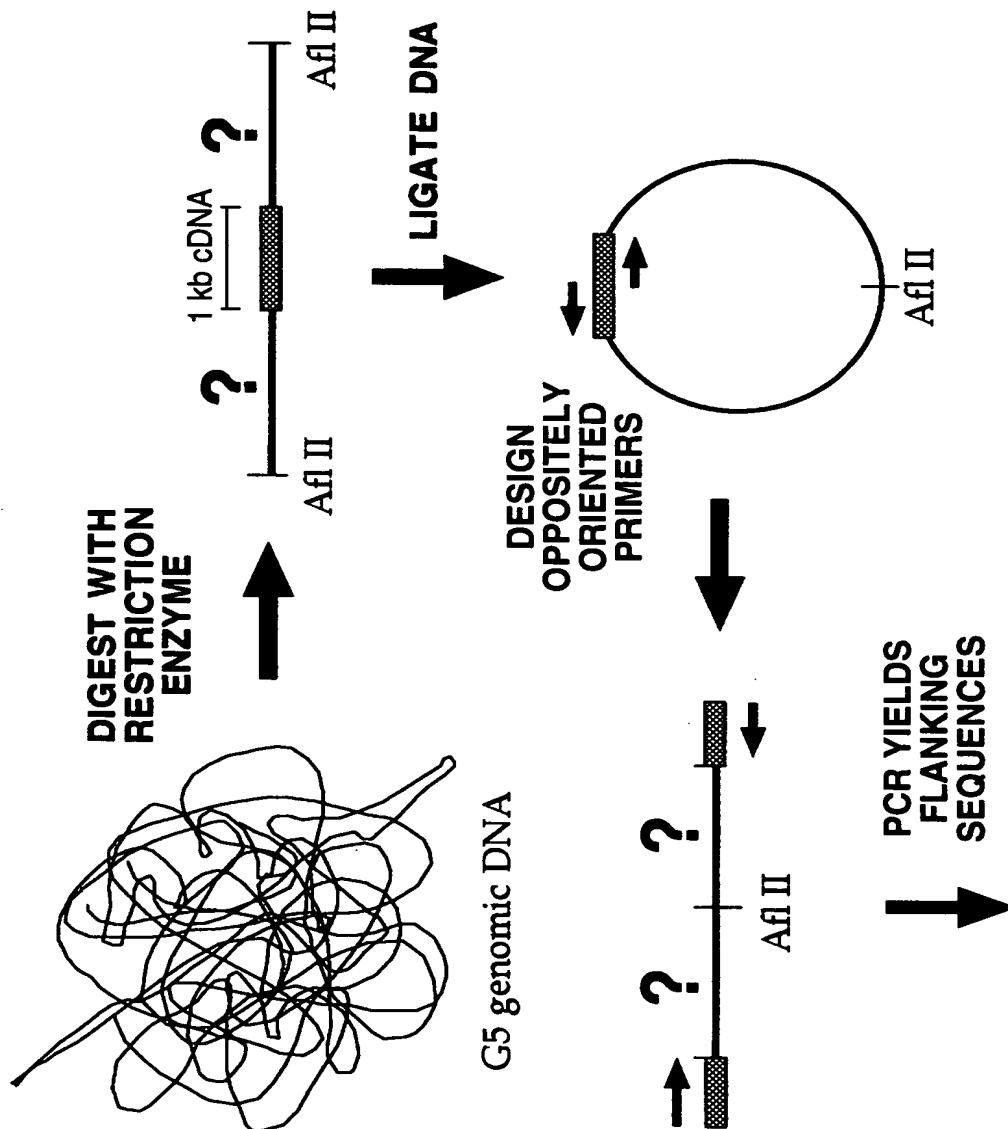
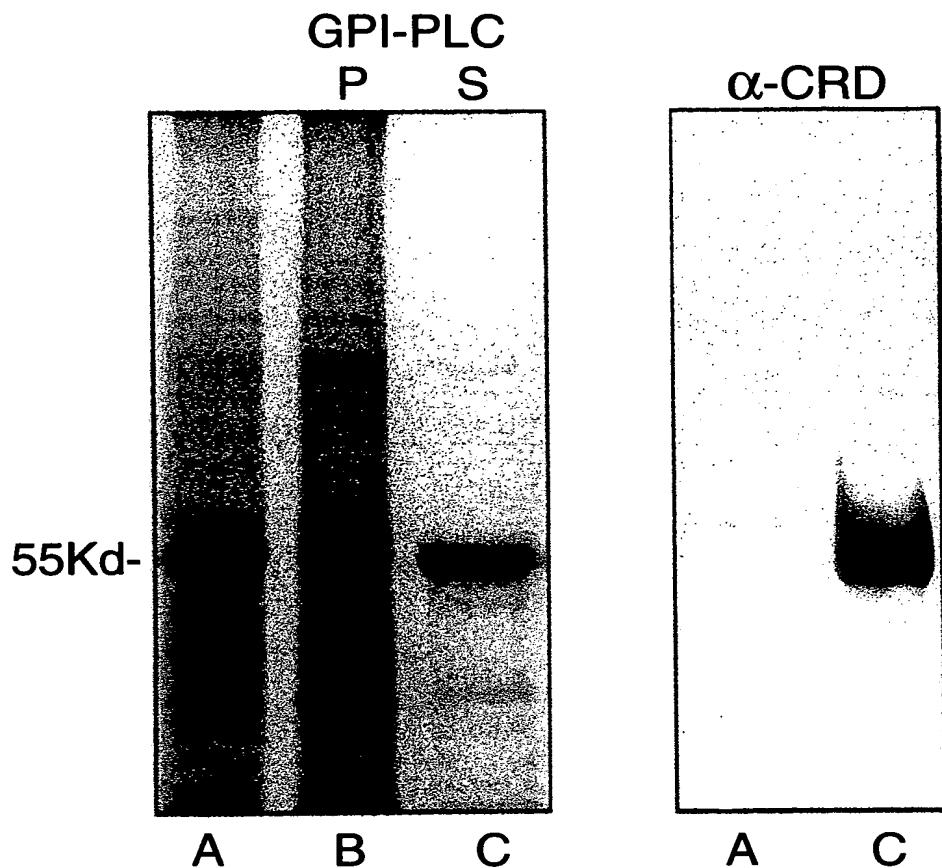


Fig. 10

15/27



*Fig. 11*

## REPLACEMENT SHEET

16/27



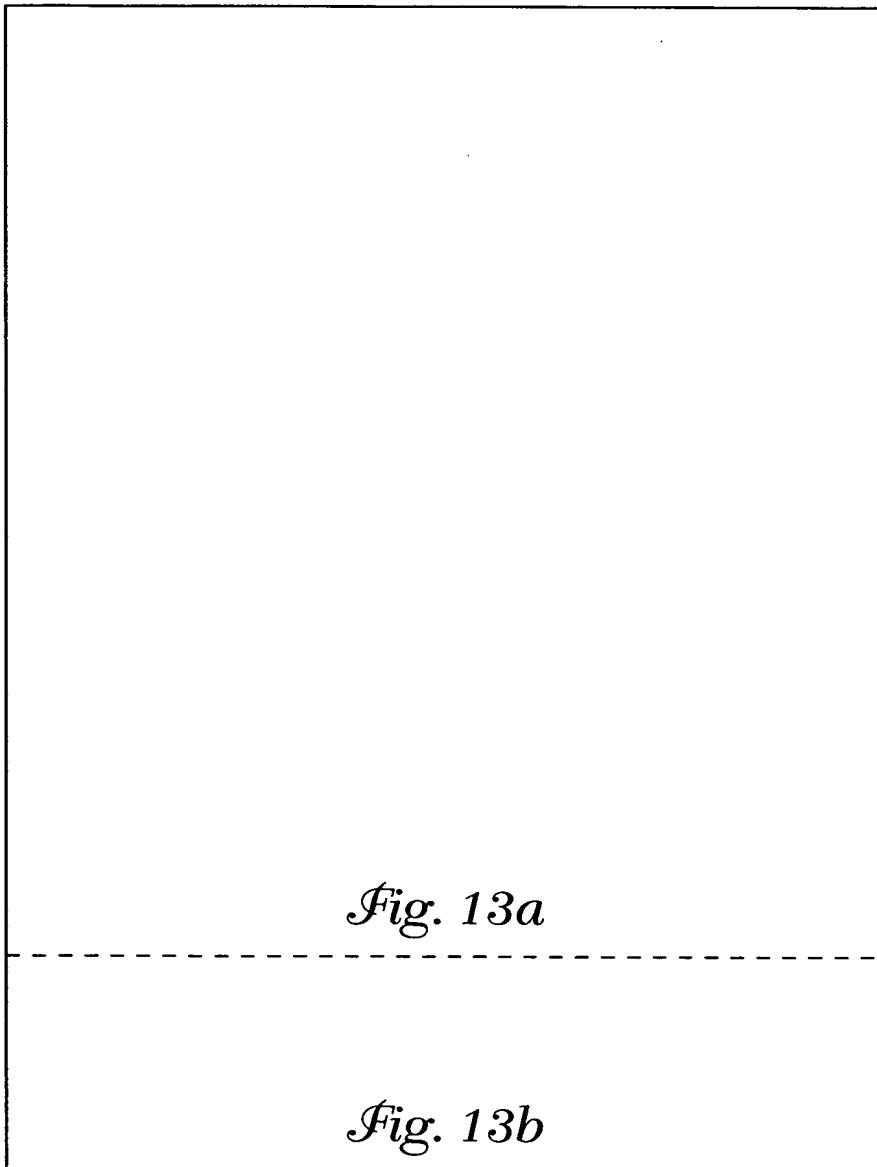
SEQ ID NO: Primers for synthesis of G5 synthetic gene.

3201:  
70 ATG GGA ATT CAA ATG AAG AAC AAC ATC CTG GTG ATC CTG ATC ATC TCT CTG TIC ATC AAC CAG ATC AAG  
TCT GCT AAC TGT CCT GTG GGA ACC GAG ACC AAC ACC GCT GGA CAG GTG  
3202:  
71 CTC CAG GCA CGA AAG CAG CAG CGT TGT TGT AGT AGA AGT TCT TCT GAC AGT TCA CAC AGT TAG CAG GGG  
TTC CCA GGT OGT CCA CCT GTC CAG CGG TGT TGG TC  
3203:  
72 CGC TGC TGC TTT CGT GCC TGG AGC TTC TAC CTG TAC CCC TTG TCC TCA GAA GAA GGA CGC TGG AGC TCA  
GCC TAA CCC TCC TGC TAC CGC TAA CCT GGT G  
3204:  
73 GAT GAT AGC AGC GTA GTC GGT AGC TCC TCC AGC GAT AGC GGT TCC AGC AGG ACA CTT CAC GTT ACA CTG  
GGT CAC CAG GTT AGC GGT AGC AGG AG  
3205:  
74 GCT ACC GAC TAC GCT GCT ATC ATC ACC GAG TGT GTG AAC TGT CGC ATC AAC TTC TAC AAC GAG AAC GCT  
CCT AAC TTC AAC GCT GGA GCT TCT ACC TGT ACC GCT TGT CCT GTG AAC CGC GTG GGA GGA GCT CTG ACC  
3206:  
75 GGT GAA AGA GCG CAC GTA GTC GGT GGT CAC TCC GTC GTC CAG AGC GGT TCC GGT AGG ACA AGC CAC GTT  
ACA CTG AGC CAC GAT GGT AGC AGC GTT TCC AGC GGT CAG AGC TCC TCC CAC GCG  
3207:  
76 GAC TAC GTG CGC TCT TTC ACC GAG TGT GTG AAG TGT OGC CTG AAC TTC TAC TAC AAC GGA AAC AAC GGA  
AAC ACC CCT TTC AAC CCT GGA AAG TCT CAG  
3208:  
77 GTG ATG GTA GCG TCG TTT CCC AGG GTA GCC TGA GCC ACG TTA GCA GGC TTG ATA GCA GGA CAA GGG GTA  
CAC TGA GAC TTT CCA GGG TTG AAA GG  
3209:  
78 GGG AAA CGA CGC TAC CAT CAC CGC TCA GTG TAA CGT GGC TTG TCC TGA CGG AAC CAT CTC TGC TGC TGG  
AGT GAA CAA CTG GGT GGC TCA GAA C  
3210:  
79 CAG ACA GGT AGA GTT TCC AGG GTT GAA GTT AGG AGC GTT GTT GTT GTA GAA GTT AGG AGC ACA GTT GGT  
ACA CTC GGT GTT CTG AGC CAC CCA GTT GTT C  
3211:  
80 CCC TGG AAA CTC TAC CTG TCT GCC TTG TCC TGC TAA CAA GGA CTA CGG AGC TGA GGC TAC CGC TAC CGC TGG AGG  
AGC TGC TAC CCT GGC TAA GC  
3212:  
81 GGT CTG CAG GAT CAC GTA GTT GGT AGC TCC AGA AGC GAT AGC GGT TCC GTC AGG ACA AGC GAT GTT ACA  
CTG CTT AGC CAG GGT AGC AGC  
3213:  
82 CAA CTA CGT GAT CCT GCA GAC CGA GTG TCT GAA CTG TGC TGC TAA CTT CTA CTT CGA CGG AAA CAA CTT  
CCA GGC TGG ATC TTC TGG CTG TAA GG  
3214:  
83 GAG CGA TCA GGG TAG CGG TTC CTC CAG CGG TAG CCA CAG CTC CCT GCA CCT TGT TAG CAG GAC AAG CCT  
TAC AGC GAG AAG ATC CAG CCT GG  
3215:  
84 GAA CGG CTA CCC TGA TCG CTC AGT GTG CTC TGG AGT GTC CTG CTG GAA CGG TGC TGA CGG ACG GAA CCA  
CCT CTA CCT ACA AGC AGG CTG CTT C  
3216:  
85 GGT GTC GAT TCC AGC CAC CGA GTC GGT CTG CTT GGT GGT GTA GAA GTT AGC AGC ACA CTT CAC ACA CTC  
AGA AGC AGC CTG CTT GTA GGT AG  
3217:  
86 GGG TGG CTG GAA TGG ACA CCT GTA CCT CTT GTA ACA AGA AGC TGA CCT CTG GAG CTG AGG CTA ACC TGC  
CTG AGT CTG CTA AGA AGA ACA TC  
3218:  
87 GAG GGA TCC TTA TTA CAG CAG GTA GTA AGA GAT CAG CAG CAG AGA GAT AGA CAG GAA GTT AGC GAA GTC  
ACA CTG GAT GTT CTT CTT AGC AGA CT

*Fig. 12*

## REPLACEMENT SHEET

17/27

*Fig. 13a**Fig. 13b**Fig. 13*

REPLACEMENT SHEET



G5 proline mutant 18/27

SEQ ID NO: 53 ATGAAGAACAA CATCCGGT GATCCTGATC ATCTCTCTGT TCATCAACCA GATCAAGTCT  
GCTAACTGTC CTGTGGAAC CGAGACCAAC ACCGCTGGAC AGGTGGACGA CCTGGGAACC  
CCTGCTAACT GTGTGAAC TG TCAGAAGAAC TTCTACTACA ACAACGCTGC TGCTTTCTGT  
CCTGGAGCTT CTACCTGTAC CCCTTGTCCT CAGAAGAAGG ACGCTGGAGC TCAGCCTAAC  
CCTCCTGCTA CCGCTAACCT GGTGACCCAG TGTAACGTGA AGTGTCCCTGC TGGAACCGCT  
ATCGCTGGAG GAGCTACCGA CTACGCTGCT ATCATCACCG AGTGTGTGAA CTGTCGCATC  
AACTTCTACA ACGAGAACGC TCCTAACCTTC AACGCTGGAG CTTCTACCTG TACCGCTTGT  
CCTGTGAACC GTGTGGGAGG AGCTCTGACC GCTGGAAACG CTGCTACCAT CGTGGCTCAG  
TGTAACGTGG CTTGCTCTAC CGGAACCGCT CTGGACGACG GAGTGACCCAC CGACTACGTG  
CGCTCTTCA CCGAGTGTGT GAAGTGTGCG CTGAACCTCT ACTACAACGG AAACAACGGA  
AACACCCCTT TCAACCCTGG AAAGTCTCAG TGTACCCCTT GTCCTGCTAT CAAGCCTGCT  
AACGTGGCTC AGGCTACCCCT GGGAAACCGAC GCTACCATCA CCGCTCAGTG TAACGTGGCT  
TGTCTGTGAG GAACCATCTC TGCTGTGGA GTGAACAACT GGGTGGCTCA GAACACCGAG  
TGTACCAACT GTGCTCCTAA CTTCTACAAAC AACAAACGTC CTAACCTCAA CCCTGGAAAC  
TCTACCTGTC TGCCCTGTCC TGCTAACAAAG GACTACGGAG CTGAGGCTAC CGCTGGAGGA  
GCTGCTACCC TGGCTAACAGA GTGTAACATC GCTTGTCTG ACGGAACCGC TATCGCTTCT  
GGAGCTACCA ACTACGTGAT CCTGCAGACC GAGTGTCTGA ACTGTGCTGC TAACTTCTAC  
TTCGACGGAA ACAACCTCCA GGCTGGATCT TCTCGCTGTG AGGCTTGTCC TGCTAACAAAG  
GTGCAGGGAG CTGTGGCTAC CGCTGGAGGA ACCGCTACCC TGATCGCTCA GTGTGCTCTG  
GAGTGTCTG CTGGAACCGT GCTGACCGAC GGAACCACCT CTACCTACAA GCAGGCTGCT  
TCTGAGTGTG TGAAGTGTGC TGCTAACCTTC TACACCACCA AGCAGACCGA CTGGGTGGCT

Fig. 13a

**REPLACEMENT SHEET**

19/27

**proline mutant**

1270 1280 1290 1300 1310 1320  
GGAATCGACA CCTGTACCTC TTGTAACAAG AAGCTGACCT CTGGAGCTGA GGCTAACCTG  
1330 1340 1350 1360 1370 1380  
CCTGAGTCTG CTAAGAAGAA CATCCAGTGT GACTTCGCTA ACTTCCTGTC TATCTCTCTG  
1390 1400 1410 1420 1430 1440  
CTGCTGATCT CTTACTACCT GCTG.....

*Fig. 13b*



REPLACEMENT SHEET

20/27



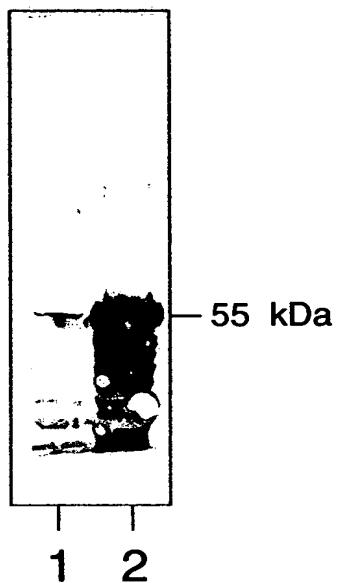
**G5 proline mutant protein**

↓ 10 20 30 40 50 60  
SEQ ID NO: 54 MKNNIPVILI ISLFINQIKS ANCPVGTETIN TAGQVDDLGT PANCVNCQKN FYYNNAAAFV  
70 80 90 100 110 120  
PGASTCTPCP QKKDAGAQPN PPATANLVTQ CNVKCPAGTA IAGGATDYAA IITECVNCRI  
130 140 150 160 170 180  
NFYNNENAPNF NAGASTCTAC PVNRVGGALT AGNAATIVAQ CNVACPTGTA LDDGVTTDYV  
190 200 210 220 230 240  
RSFTECVKCR LNFYYNGNNG NTPFNPNGKSQ CTPCPAIKPA NVAQATLGND ATITAQCNVA  
250 260 270 280 290 300  
CPDGTISAAG VNNWVAQNT ECTNCAPNFYN NNAPNFNPNG STCLPCPANK DYGAETAGG  
310 320 330 340 350 360  
AATLAKQCNI ACPDGTAIAS GATNYVILQT ECLNCAANFY FDGNNFQAGS SRCKACPANK  
370 380 390 400 410 420  
VQGAVATAGG TATLIAQCAL ECPAGTVLTD GTTSTYKQAA SECVKCAANF YTTKQTDWVA  
430 440 450 460 470 480  
GIDTCTSCNK KLTSGAEANL PESAKKNIQC DFANFLSISL LLISYYLL... ....

*Fig. 14*

**REPLACEMENT SHEET**

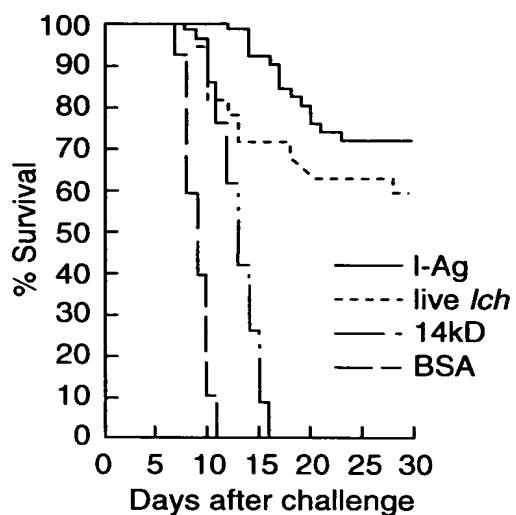
21/27



*Fig. 15*

**REPLACEMENT SHEET**

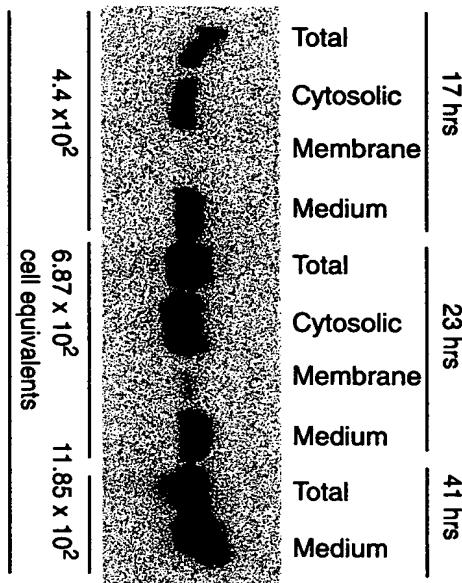
22/27



*Fig. 16*

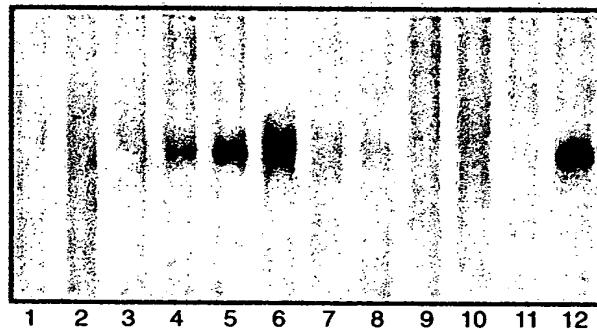
**REPLACEMENT SHEET**

23/27



*Fig. 17*

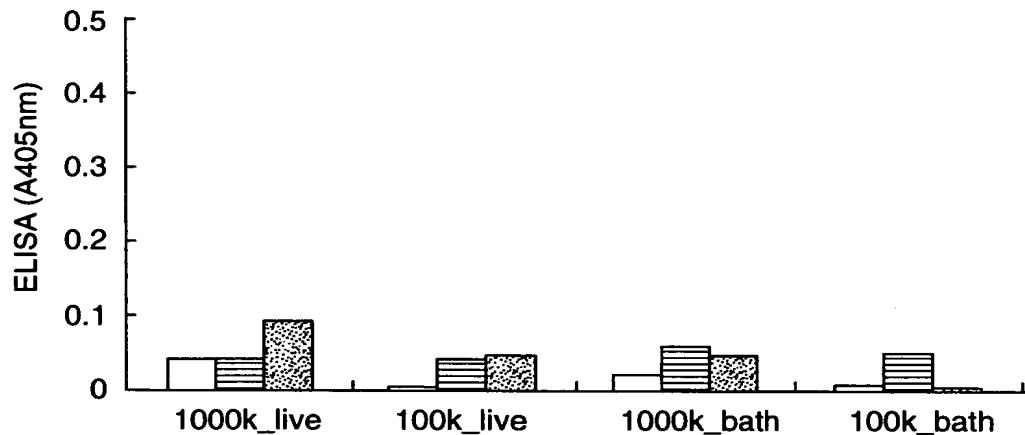
24/27



*Fig. 18*

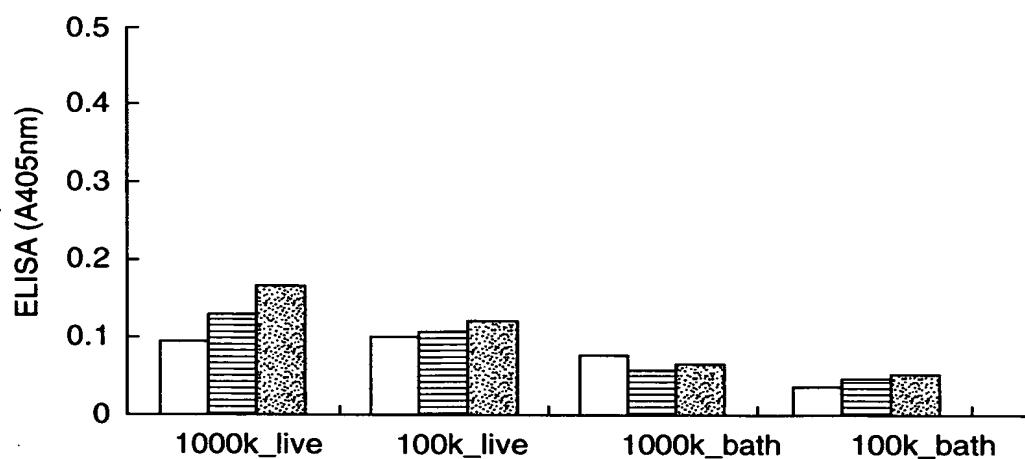
REPLACEMENT SHEET

25/27



*Fig. 19a*

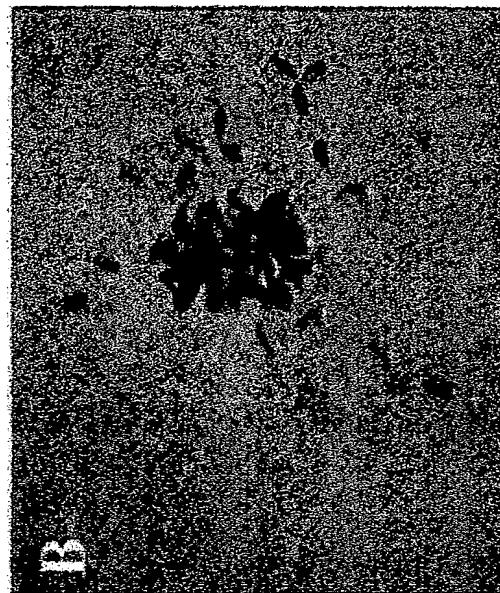
- Week 2
- ▨ Week 4
- ▨ Week 6



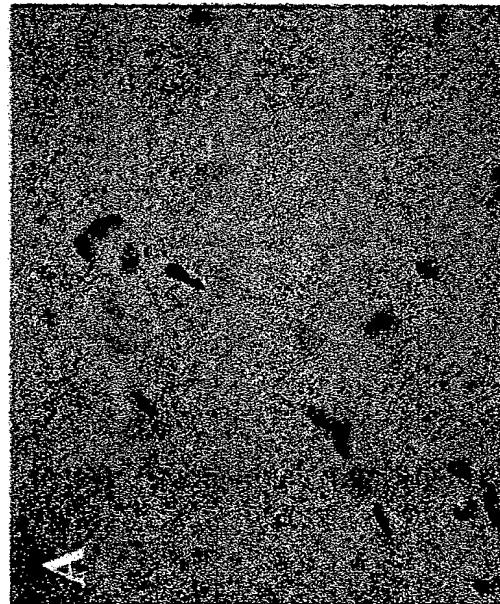
*Fig. 19b*

- Week 2
- ▨ Week 4
- ▨ Week 6

26/27



Serum: anti-live TG1 (1 : 20)



Serum: anti-live Theo (1 : 20)  
(negative control)

*Fig. 20b*

*Fig. 20a*

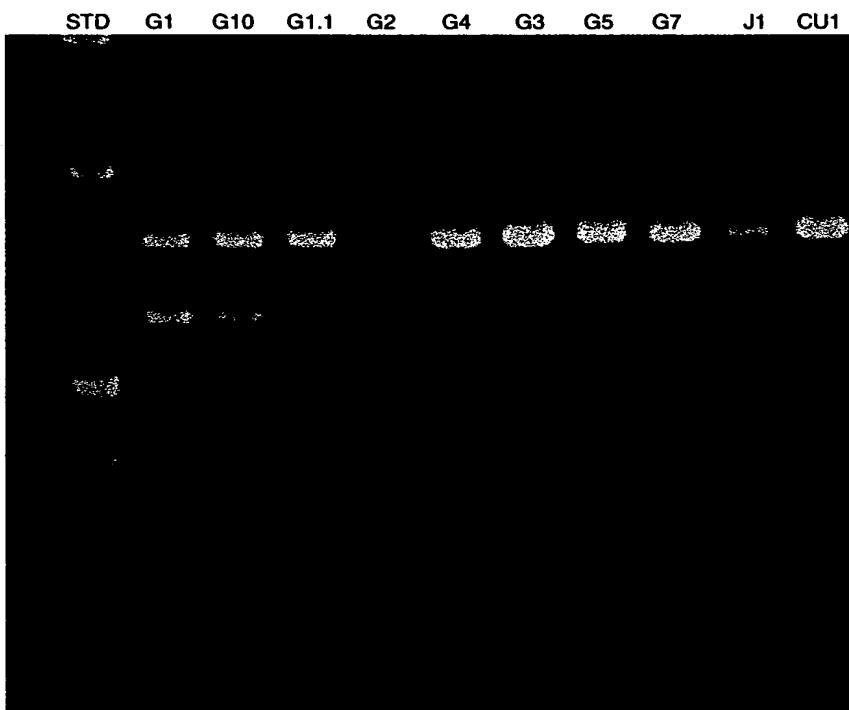
Title: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF ICHTHYOPHTHIRIUS  
Applicant(s): CLARK et al.  
Serial No.: 09/497,967

Filed: February 4, 2000

**REPLACEMENT SHEET**

Docket: 235.0017 0101  
Sheet 27 of 27

27/27



*Fig. 21*